

0128
RAW SEQUENCE LISTING
PATENT APPLICATION US/09/012,846

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DATE: 02/23/98
TIME: 15:29:20

INPUT SET: S23737.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Marc F. Charette
6
7 (ii) TITLE OF INVENTION: Methods and Compositions for Enhancing Cognitive Func
8
9 (iii) NUMBER OF SEQUENCES: 9
10
11 (iv) CORRESPONDENCE ADDRESS:
12 (A) ADDRESSEE: CREATIVE BIOMOLECULES, INC
13 (B) STREET: 45 SOUTH STREET
14 (C) CITY: HOPKINTON
15 (D) STATE: MA
16 (E) COUNTRY: USA
17 (F) ZIP: 01748
18
19 (v) COMPUTER READABLE FORM:
20 (A) MEDIUM TYPE: Floppy disk
21 (B) COMPUTER: IBM PC compatible
22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
24
25 (vi) CURRENT APPLICATION DATA:
26 (A) APPLICATION NUMBER:
27 (B) FILING DATE:
28 (C) CLASSIFICATION:
29
30 (viii) ATTORNEY/AGENT INFORMATION:
31 (A) NAME: Thomas C. Meyers
32 (B) REGISTRATION NUMBER:
33 (C) REFERENCE/DOCKET NUMBER: CRP-141
34
35 (ix) TELECOMMUNICATION INFORMATION:
36 (A) TELEPHONE: (617) 248-7000
37 (B) TELEFAX: (617) 248-7100
38
39
40 (2) INFORMATION FOR SEQ ID NO:1:
41
42 (i) SEQUENCE CHARACTERISTICS:
43 (A) LENGTH: 1822 base pairs
44 (B) TYPE: nucleic acid
45 (C) STRANDEDNESS: single
46 (D) TOPOLOGY: linear

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47
48 (ii) MOLECULE TYPE: cDNA
49
50 (vi) ORIGINAL SOURCE:
51 (A) ORGANISM: HOMO SAPIENS
52 (F) TISSUE TYPE: HIPPOCAMPUS
53
54 (ix) FEATURE:
55 (A) NAME/KEY: CDS
56 (B) LOCATION: 49..1341
57 (C) IDENTIFICATION METHOD: experimental
58 (D) OTHER INFORMATION: /function= "MORPHOGENIC PROTEIN"
59 /product= "OP1"
60 /evidence= EXPERIMENTAL
61 /standard_name= "OP1"
62
63
64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
65
66 GGTGCGGGCC CGGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG      57
67                                     Met His Val
68                                     1
69
70 CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA      105
71 Arg Ser Leu Arg Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
72     5              10              15
73
74 CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC      153
75 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
76   20              25              30              35
77
78 GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG      201
79 Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
80               40              45              50
81
82 CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC      249
83 Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
84           55              60              65
85
86 CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG      297
87 Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
88       70              75              80
89
90 CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC      345
91 Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly
92   85              90              95
93
94 GGC CAG GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC      393
95 Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
96  100              105              110              115
97
98 CCC CCT CTG GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC      441
99 Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp

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	120	125	130	
100				
101				
102	ATG GTC ATG AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC			489
103	Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe			
104		135	140	145
105				
106	CAC CCA CGC TAC CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC			537
107	His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile			
108		150	155	160
109				
110	CCA GAA GGG GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC			585
111	Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp			
112		165	170	175
113				
114	TAC ATC CGG GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT			633
115	Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr			
116	180	185	190	195
117				
118	CAG GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC			681
119	Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu			
120		200	205	210
121				
122	GAC AGC CGT ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT GAC			729
123	Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp			
124		215	220	225
125				
126	ATC ACA GCC ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC AAC CTG			777
127	Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu			
128		230	235	240
129				
130	GGC CTG CAG CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC ATC AAC CCC			825
131	Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro			
132		245	250	255
133				
134	AAG TTG GCG GGC CTG ATT GGG CGG CAC GGG CCC CAG AAC AAG CAG CCC			873
135	Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro			
136	260	265	270	275
137				
138	TTC ATG GTG GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CGC AGC ATC			921
139	Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile			
140		280	285	290
141				
142	CGG TCC ACG GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG CCC			969
143	Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro			
144		295	300	305
145				
146	AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC GTG GCA GAG AAC AGC AGC			1017
147	Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser			
148		310	315	320
149				
150	AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC			1065
151	Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe			
152		325	330	335

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153
154 CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC 1113
155 Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala
156 340 345 350 355
157
158 GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG 1161
159 Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met
160 360 365 370
161
162 AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC 1209
163 Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn
164 375 380 385
165
166 CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC 1257
167 Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala
168 390 395 400
169
170 ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA 1305
171 Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys
172 405 410 415
173
174 TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC 1351
175 Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
176 420 425 430
177
178 GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CTTTGGCCAG 1411
179
180 GAACCAGCAG ACCAACTGCC TTTTGTGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG 1471
181
182 TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCAGTTTTT CAGTGGCAGC 1531
183
184 ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAACC TAGCAGGAAA AAAAAACAAC 1591
185
186 GCATAAAGAA AAATGGCCGG GCCAGGTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT 1651
187
188 CGTTTCCAGA GGTAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG 1711
189
190 GGCGTGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAAG GAAAATTGAC CCGGAAGTTC 1771
191
192 CTGTAATAAA TGTCAATAA AAACGAATGA ATGAAAAAAAA AAAAAAAAAA A 1822
193
194

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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206 Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
207   1                      5                      10                      15
208
209 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
210                20                25                30
211
212 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
213       35                40                45
214
215 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
216       50                55                60
217
218 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
219   65                70                75                80
220
221 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
222                85                90                95
223
224 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
225       100                105                110
226
227 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
228       115                120                125
229
230 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
231   130                135                140
232
233 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
234   145                150                155                160
235
236 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
237       165                170                175
238
239 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
240       180                185                190
241
242 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
243       195                200                205
244
245 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
246       210                215                220
247
248 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
249   225                230                235                240
250
251 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
252       245                250                255
253
254 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
255       260                265                270
256
257 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
258       275                280                285

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SEQUENCE VERIFICATION REPORT
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Original Text